

Does Not Comply  
Corrected Diskette Needed  
See Additional pages 1 & 2  
See extra page 1



1632

## RAW SEQUENCE LISTING

DATE: 06/05/2002

PATENT APPLICATION: US/09/731,261

TIME: 10:14:17

Input Set : A:\ptoms.TXT

Output Set: N:\CRF3\06052002\I731261.raw

3 <110> APPLICANT: Habener, Joel  
4 Zulewski, Hendrik  
5 Abraham, Elizabeth  
6 Vallejo, Mario  
8 <120> TITLE OF INVENTION: STEM CELLS OF THE ISLETS OF LANGERHANS AND THEIR USE IN  
TREATING DIABETES

9 MELLITUS

11 &lt;130&gt; FILE REFERENCE: 3284/1230

13 &lt;140&gt; CURRENT APPLICATION NUMBER: US 09/731,261

14 &lt;141&gt; CURRENT FILING DATE: 2000-12-06

16 &lt;150&gt; PRIOR APPLICATION NUMBER: US 60/169,082

17 &lt;151&gt; PRIOR FILING DATE: 1999-12-06

19 &lt;150&gt; PRIOR APPLICATION NUMBER: US 60/215,109

20 &lt;151&gt; PRIOR FILING DATE: 2000-06-28

22 &lt;150&gt; PRIOR APPLICATION NUMBER: US 60/239,880

23 &lt;151&gt; PRIOR FILING DATE: 2000-10-06

25 &lt;160&gt; NUMBER OF SEQ ID NOS: 55

27 &lt;170&gt; SOFTWARE: PatentIn version 3.1

29 &lt;210&gt; SEQ ID NO: 1

30 &lt;211&gt; LENGTH: 4854

31 &lt;212&gt; TYPE: DNA

32 &lt;213&gt; ORGANISM: Homo sapiens

34 &lt;400&gt; SEQUENCE: 1

35	atggagggct	gcatggggga	ggagtcgttt	cagatgtggg	agctcaatcg	gcgcctggag	60
37	gcctacctgg	gccgggtcaa	ggcgctggag	gagcagaatg	agctgctcag	cgccggactc	120
39	ggggggctcc	ggcgacaatc	cgcggaacac	tcctggcggg	cgcatgccga	cgacgagctg	180
41	gcggccctgc	gtgcgctcgt	tgaccaacgc	tggcgggaga	agcacgcggc	cgaggtggcg	240
43	cgcgacaacc	tggctgaaga	gctggagggc	gtggcaggcc	gatgcgagca	gctgcggctg	300
45	gcccgggagc	ggacgacgga	ggaggtagcc	cgcaaccggc	gcgccgtcga	ggcagagaaa	360
47	tgcgcccggg	cctggctgag	tagccagggg	gcagagctgg	agcgcgagct	agaggctcta	420
49	cgcgctggcg	acgaggagga	gcgcgtcggt	ctgaacgcgc	aggctgcctg	tgccccccgc	480
51	ctgccccgcg	cgccccggcc	tccccgcgcc	gccccggagg	tagaggagct	ggcaaggcga	540
53	ctgggcgagg	cgtggcgcg	ggcagtgcgc	ggctaccagg	agcgcggtgg	acacatggag	600
55	acgtcgctgg	accagaccgc	cgagcgctg	gccccggcgg	tgagggtg	ccgcgaggtc	660
57	cgctggagc	tgacgagct	ccaggctgag	cgcgaggcc	tcctggagcg	cagggcagcg	720
59	ttggaacaga	ggttgagg	ccgctggcag	gagcggtcgc	gggctactga	aaagtccag	780
61	ctggctgtgg	aggccctgga	gcaggagaaa	cagggcctac	agagccagat	cgctcaggtc	840
63	ctggaaggtc	ggcagcagct	ggcgacacct	aagatgtccc	tcagccctga	ggtggccacg	900
65	tacaggacct	tcctggagcc	tgagaaactc	cggtgcgaaa	cacctggcgg	tggctccaag	960
67	acttccctca	gctttcagga	ccccaaactg	gagctgcaat	tccttaggac	cccagagggc	1020
69	cggcgtcttg	gatctttgct	cccagtcctg	agccccactt	ccctccccct	acccttgcc	1080
71	gctacccttg	agacacctgt	gccagccttt	cttaagaacc	aagaattcct	ccaggccccg	1140
73	accctacct	tggccagcac	ccccatcccc	cccacacctc	aggcaccctc	tcctgctgta	1200
75	gatgcagaga	tcagagccca	ggatgctcct	ctctctctgc	tccagacaca	gggtgggagg	1260

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77	aaacaggctc	cagagccccct	gcgggctgaa	gccaggggtgg	ccattcctgc	cagcgtcctg	1320
79	cctggaccag	aggagcctgg	gggccagcgg	caagaggcca	gtacaggcca	gtccccagag	1380
81	gaccatgcct	ccttggcacc	accctcagc	cctgaccact	ccagtttaga	ggctaaggat	1440
83	ggagaatccg	gtgggtctag	agtgttcagc	atatgccgag	gggaaggtag	agggcaaadc	1500
85	tgggggttgg	tagagaaaag	aacagccata	gagggcaaac	tggttagcag	cttgacagag	1560
87	gaaatatggg	aagaagagga	tctaaacagg	aaggaaatcc	aggactcccc	ggttcctttg	1620
89	gaaaaagaaa	ccctgaagtc	tctgggagag	gagattcaag	agtcactgaa	gactctggaa	1680
91	aaccagagcc	atgagacact	agaaagggag	aatcaagaat	gtccgaggtc	tttagaagaa	1740
93	gacttagaaa	cactaaaaag	tctagaaaaa	gaaaataaaa	gagctattaa	aggatgtgga	1800
95	ggtagtgaga	cctctagaaa	aagaggctgt	aggcaactta	agcctacagg	aaaagaggac	1860
97	acacagacat	tgcaatccct	gcaaaaggag	aatcaagaac	taatgaaatc	tcttgaaggt	1920
99	aatctagaga	cattttttatt	tccaggaacg	gaaaatcaag	aattagtaag	ttctctgcaa	1980
101	gagaacttag	agtcattgac	agctctggaa	aaggagaatc	aagagccact	gagatctcca	2040
103	gaagtagggg	atgaggaggc	actgagacct	ctgacaaagg	agaatcagga	accctgaggg	2100
105	tctcttgaag	atgagaacaa	agaggccttt	agatctctag	aaaaagagaa	ccaggagcca	2160
107	ctgaagactc	tagaagaaga	ggaccagagt	attgtgagac	ctctagaaac	agagaatcac	2220
109	aaatcactga	ggtcttttag	agaacaggac	caagagacat	tgagaactct	tgaaaaagag	2280
111	actcaacagc	gacggaggtc	tctaggggaa	caggatcaga	tgacattaag	acccccagaa	2340
113	aaagtggatc	tagaaccact	gaagtctctt	gaccaggaga	tagctagacc	tcttgaaaat	2400
115	gagaatcaag	agttctttaa	gtcactcaaa	gaagagagcg	tagaggcagt	aaaatcttta	2460
117	gaaacagaga	tcctagaatc	actgaagtct	gcgggacaag	agaacctgga	aacactgaaa	2520
119	tctccagaaa	ctcaagcacc	actgtggact	ccagaagaaa	taaataaatc	agggggcaat	2580
121	gaatcctcta	gaaaaggaaa	ttcaagaacc	actggagtct	gtggaagtga	accaagagac	2640
123	attcagactc	ctggaagagg	agaatcagga	atcattgaga	tctctgggag	catggaacct	2700
125	ggagaatttg	agatctccag	aggagtagac	aaggaaaagtc	aaaggaatct	ggaagaggaa	2760
127	gagaacctgg	gaaagggaga	gtaccaagag	tcaactgagg	ctctggaggga	ggaggggacg	2820
129	gagctgccgc	agctctgaga	tgtgcagagg	tggaagata	cggtggagaa	ggaccaagaa	2880
131	ctggctcagg	aaagccctcc	tgggatggct	ggagtggaaa	ataaggatga	ggcagagctg	2940
133	aatctaaggg	agcaggatgg	cttcaactgg	aaggaggagg	tggttagagca	gggagagctg	3000
135	aatgccacag	aggaggtctg	gttcccaggc	gaggggcacc	cagagaaccc	tgagcccaaa	3060
137	gagcagagag	gcctgggttg	gggagccagt	gtgaaggagg	gggctgaggg	cctccaggac	3120
139	cctgaagggc	aatcacaaca	ggtggggacc	ccaggcctcc	aggctcccca	ggggctgcca	3180
141	gaggcgatag	agcccctgg	ggaagatgat	gtggcccag	ggggtgacca	agcctcccca	3240
143	gaggtcatgt	tggggtcaga	gcctgccatg	ggtgagtctg	ctgcgggagc	tgagccaggc	3300
145	ctggggcagg	gggtgggagg	gctgggggac	ccaggccatc	tgaccaggga	agaggtgatg	3360
147	gaaccacccc	tggaagagga	gagtttgagg	gcaaaagggg	ttcagggctt	ggaagggcct	3420
149	agaaaggacc	tagaggaggc	aggtggtctg	gggacagagt	tctccgagct	gcctggggaag	3480
151	agcagagacc	cttgggagcc	tcccaggagg	ggtaggaggg	agtcagaggc	tgaggccccc	3540
153	aggggagcag	aggaggcgtt	ccctgctgag	accctgggcc	acactggaag	tgatgccctt	3600
155	tcaccttggc	ctctggggtc	agaggaagct	gaggaggatg	taccaccagt	gctggtctcc	3660
157	cccagcccaa	cgtacacccc	gaccttgga	gatgccctg	ggctccagcc	tcaggctgaa	3720
159	gggagtcagg	aggctagctg	gggggtgcag	gggagggctg	aagctgggaa	agtagagagc	3780
161	gagcaggagg	agttgggttc	tggggagatc	cccgagggcc	tccaggagga	aggggaggag	3840
163	agcagagaag	agatgagag	ggatgagctc	ggggagaccc	ttccagactc	cactcccttg	3900
165	gccttctacc	tcagggtccc	cacctccccc	aggtggaccc	cactggagag	cagaggccac	3960
167	cccctcaagg	agactggaag	ggagggctgg	gatcctgctg	tcctggcttc	cgagggcctt	4020
169	gaggaacctt	cagaaaagga	ggagggggag	gagggagaag	aggagtgtgg	ccgtgactct	4080
171	gacctgtcag	aagaatttga	ggacctgggg	actgaggcac	cttttcttcc	tggggctcct	4140
173	ggggagggtg	cagaacctct	gggccagggt	ccccagctgc	tactggatcc	tgacgcttgg	4200

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PATENT APPLICATION: US/09/731,261

DATE: 06/05/2002

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Input Set : A:\ptoms.TXT

Output Set: N:\CRF3\06052002\I731261.raw

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175 gatcgagatg gggagtctga tgggttttgca gatgaggaag aaagtgggga ggagggagag 4260
177 gaggatcagg aggaggggag ggagccagg gctgggcggt gggggccagg gtcttctgtt 4320
179 ggcagcctcc aggccttgag tagctcccag agaggggaat tcctggagtc tgattctgta 4380
181 agtgtcagcg tcccctggga tgacagcttg aggggtgcag tggttggtgc cccaagact 4440
183 gccctggaaa cggagtccca ggacagtgtc gagccttctg gctcagagga agagtctgac 4500
185 cctgtttcct tggagaggga ggacaaagtc cctggccctc tagagatccc cagtgggatg 4560
187 gaggatgcag gcccaggggc agacatcatt ggtgttaatg gccaggggtcc caacttgag 4620
189 gggaagtcac agcatgtaaa tgggggagta atgaacgggc tggagcagtc tgaggaaagt 4680
191 ggggcaagga atgcgctagt ctctgaggga gaccgagggga gcccctttca ggaggaggag 4740
193 gggagtgtc tgaagagggtc ttccggcagg gctcctgttc acctgggcca gggtcagttc 4800
195 ctgaagtcca ctccagaggga aggagataga gagtccctgtt cctcagggga ggac 4854
198 <210> SEQ ID NO: 2
199 <211> LENGTH: 1618
200 <212> TYPE: PRT
201 <213> ORGANISM: Homo sapiens
203 <400> SEQUENCE: 2
205 Met Glu Gly Cys Met Gly Glu Glu Ser Phe Gln Met Trp Glu Leu Asn
206 1 5 10 15
209 Arg Arg Leu Glu Ala Tyr Leu Gly Arg Val Lys Ala Leu Glu Glu Gln
210 20 25 30
213 Asn Glu Leu Leu Ser Ala Gly Leu Gly Gly Leu Arg Arg Gln Ser Ala
214 35 40 45
217 Asp Thr Ser Trp Arg Ala His Ala Asp Asp Glu Leu Ala Ala Leu Arg
218 50 55 60
221 Ala Leu Val Asp Gln Arg Trp Arg Glu Lys His Ala Ala Glu Val Ala
222 65 70 75 80
225 Arg Asp Asn Leu Ala Glu Glu Leu Glu Gly Val Ala Gly Arg Cys Glu
226 85 90 95
229 Gln Leu Arg Leu Ala Arg Glu Arg Thr Thr Glu Glu Val Ala Arg Asn
230 100 105 110
233 Arg Arg Ala Val Glu Ala Glu Lys Cys Ala Arg Ala Trp Leu Ser Ser
234 115 120 125
237 Gln Gly Ala Glu Leu Glu Arg Glu Leu Glu Ala Leu Arg Val Ala His
238 130 135 140
241 Glu Glu Glu Arg Val Gly Leu Asn Ala Gln Ala Ala Cys Ala Pro Arg
242 145 150 155 160
245 Leu Pro Ala Pro Pro Arg Pro Pro Ala Pro Ala Pro Glu Val Glu Glu
246 165 170 175
249 Leu Ala Arg Arg Leu Gly Glu Ala Trp Arg Gly Ala Val Arg Gly Tyr
250 180 185 190
253 Gln Glu Arg Val Ala His Met Glu Thr Ser Leu Asp Gln Thr Arg Glu
254 195 200 205
257 Arg Leu Ala Arg Ala Val Gln Gly Ala Arg Glu Val Arg Leu Glu Leu
258 210 215 220
261 Gln Gln Leu Gln Ala Glu Arg Gly Gly Leu Leu Glu Arg Arg Ala Ala
262 225 230 235 240
265 Leu Glu Gln Arg Leu Glu Gly Arg Trp Gln Glu Arg Leu Arg Ala Thr
266 245 250 255
269 Glu Lys Phe Gln Leu Ala Val Glu Ala Leu Glu Gln Glu Lys Gln Gly

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270	260	265	270
273 Leu Gln Ser Gln Ile Ala Gln Val Leu Glu Gly Arg Gln Gln Leu Ala			
274	275	280	285
277 His Leu Lys Met Ser Leu Ser Leu Glu Val Ala Thr Tyr Arg Thr Leu			
278	290	295	300
281 Leu Glu Ala Glu Asn Ser Arg Leu Gln Thr Pro Gly Gly Ser Lys			
282 305	310	315	320
285 Thr Ser Leu Ser Phe Gln Asp Pro Lys Leu Glu Leu Gln Phe Pro Arg			
286	325	330	335
289 Thr Pro Glu Gly Arg Arg Leu Gly Ser Leu Leu Pro Val Leu Ser Pro			
290	340	345	350
293 Thr Ser Leu Pro Ser Pro Leu Pro Ala Thr Leu Glu Thr Pro Val Pro			
294	355	360	365
297 Ala Phe Leu Lys Asn Gln Glu Phe Leu Gln Ala Arg Thr Pro Thr Leu			
298	370	375	380
301 Ala Ser Thr Pro Ile Pro Pro Thr Pro Gln Ala Pro Ser Pro Ala Val			
302 385	390	395	400
305 Asp Ala Glu Ile Arg Ala Gln Asp Ala Pro Leu Ser Leu Leu Gln Thr			
306	405	410	415
309 Gln Gly Gly Arg Lys Gln Ala Pro Glu Pro Leu Arg Ala Glu Ala Arg			
310	420	425	430
313 Val Ala Ile Pro Ala Ser Val Leu Pro Gly Pro Glu Glu Pro Gly Gly			
314	435	440	445
317 Gln Arg Gln Glu Ala Ser Thr Gly Gln Ser Pro Glu Asp His Ala Ser			
318	450	455	460
321 Leu Ala Pro Pro Leu Ser Pro Asp His Ser Ser Leu Glu Ala Lys Asp			
322 465	470	475	480
325 Gly Glu Ser Gly Gly Ser Arg Val Phe Ser Ile Cys Arg Gly Glu Gly			
326	485	490	495
329 Glu Gly Gln Ile Trp Gly Leu Val Glu Lys Glu Thr Ala Ile Glu Gly			
330	500	505	510
333 Lys Val Val Ser Ser Leu Gln Gln Glu Ile Trp Glu Glu Glu Asp Leu			
334	515	520	525
337 Asn Arg Lys Glu Ile Gln Asp Ser Gln Val Pro Leu Glu Lys Glu Thr			
338	530	535	540
341 Leu Lys Ser Leu Gly Glu Glu Ile Gln Glu Ser Leu Lys Thr Leu Glu			
342 545	550	555	560
345 Asn Gln Ser His Glu Thr Leu Glu Arg Glu Asn Gln Glu Cys Pro Arg			
346	565	570	575
349 Ser Leu Glu Glu Asp Leu Glu Thr Leu Lys Ser Leu Glu Lys Glu Asn			
350	580	585	590
353 Lys Arg Ala Ile Lys Gly Cys Gly Gly Ser Glu Thr Ser Arg Lys Arg			
354	595	600	605
357 Gly Cys Arg Gln Leu Lys Pro Thr Gly Lys Glu Asp Thr Gln Thr Leu			
358	610	615	620
361 Gln Ser Leu Gln Lys Glu Asn Gln Glu Leu Met Lys Ser Leu Glu Gly			
362 625	630	635	640
365 Asn Leu Glu Thr Phe Leu Phe Pro Gly Thr Glu Asn Gln Glu Leu Val			
366	645	650	655

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369 Ser Ser Leu Gln Glu Asn Leu Glu Ser Leu Thr Ala Leu Glu Lys Glu
370          660          665          670
373 Asn Gln Glu Pro Leu Arg Ser Pro Glu Val Gly Asp Glu Glu Ala Leu
374          675          680          685
377 Arg Pro Leu Thr Lys Glu Asn Gln Glu Pro Leu Arg Ser Leu Glu Asp
378          690          695          700
381 Glu Asn Lys Glu Ala Phe Arg Ser Leu Glu Lys Glu Asn Gln Glu Pro
382 705          710          715          720
385 Leu Lys Thr Leu Glu Glu Asp Gln Ser Ile Val Arg Pro Leu Glu
386          725          730          735
389 Thr Glu Asn His Lys Ser Leu Arg Ser Leu Glu Glu Gln Asp Gln Glu
390          740          745          750
393 Thr Leu Arg Thr Leu Glu Lys Glu Thr Gln Gln Arg Arg Arg Ser Leu
394          755          760          765
397 Gly Glu Gln Asp Gln Met Thr Leu Arg Pro Pro Glu Lys Val Asp Leu
398          770          775          780
401 Glu Pro Leu Lys Ser Leu Asp Gln Glu Ile Ala Arg Pro Leu Glu Asn
402 785          790          795          800
405 Glu Asn Gln Glu Phe Leu Lys Ser Leu Lys Glu Glu Ser Val Glu Ala
406          805          810          815
409 Val Lys Ser Leu Glu Thr Glu Ile Leu Glu Ser Leu Lys Ser Ala Gly
410          820          825          830
413 Gln Glu Asn Leu Glu Thr Leu Lys Ser Pro Glu Thr Gln Ala Pro Leu
414          835          840          845
417 Trp Thr Pro Glu Glu Ile Asn Lys Ser Gly Gly Asn Glu Ser Ser Arg
418          850          855          860
421 Lys Gly Asn Ser Arg Thr Thr Gly Val Cys Gly Ser Glu Pro Arg Asp
422 865          870          875          880
425 Ile Gln Thr Pro Gly Arg Gly Glu Ser Gly Ile Ile Glu Ile Ser Gly
426          885          890          895
429 Ser Met Glu Pro Gly Glu Phe Glu Ile Ser Arg Gly Val Asp Lys Glu
430          900          905          910
433 Ser Gln Arg Asn Leu Glu Glu Glu Glu Asn Leu Gly Lys Gly Glu Tyr
434          915          920          925
437 Gln Glu Ser Leu Arg Ser Leu Glu Glu Glu Gly Gln Glu Leu Pro Gln
438          930          935          940
441 Ser Ala Asp Val Gln Arg Trp Glu Asp Thr Val Glu Lys Asp Gln Glu
442 945          950          955          960
445 Leu Ala Gln Glu Ser Pro Pro Gly Met Ala Gly Val Glu Asn Lys Asp
446          965          970          975
449 Glu Ala Glu Leu Asn Leu Arg Glu Gln Asp Gly Phe Thr Gly Lys Glu
450          980          985          990
453 Glu Val Val Glu Gln Gly Glu Leu Asn Ala Thr Glu Glu Val Trp Phe
454          995          1000          1005
457 Pro Gly Glu Gly His Pro Glu Asn Pro Glu Pro Lys Glu Gln Arg
458          1010          1015          1020
461 Gly Leu Val Glu Gly Ala Ser Val Lys Gly Gly Ala Glu Gly Leu
462          1025          1030          1035
465 Gln Asp Pro Glu Gly Gln Ser Gln Gln Val Gly Thr Pro Gly Leu

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 8

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29

Seq#:30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53

Seq#:54,55

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"  
or "Unknown". Please explain source of genetic material in <220> to <223>  
section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)  
(Sec.1.823 of new Rules)

Seq#:7

## VERIFICATION SUMMARY

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Input Set : A:\ptoms.TXT

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L:624 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
L:627 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3  
L:639 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
L:642 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4  
L:654 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:657 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
L:669 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:672 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6  
L:684 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
L:686 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:686 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:693 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:696 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8  
L:708 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
L:711 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9  
L:723 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10  
L:726 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10  
L:738 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11  
L:741 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11  
L:753 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12  
L:756 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12  
L:768 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13  
L:771 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13  
L:783 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14  
L:786 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14  
L:798 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15  
L:801 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:813 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16  
L:816 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16  
L:828 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17  
L:831 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17  
L:843 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18  
L:846 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18  
L:858 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19  
L:861 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19  
L:873 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20  
L:876 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20  
L:888 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21  
L:891 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21  
L:903 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22  
L:906 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22  
L:918 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23  
L:921 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23  
L:933 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24  
L:936 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24  
L:948 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25  
L:951 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25  
L:963 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/731,261

DATE: 06/05/2002

TIME: 10:14:18

Input Set : A:\ptoms.TXT

Output Set: N:\CRF3\06052002\I731261.raw

L:966 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26  
L:978 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27  
L:981 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27  
L:993 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28  
L:996 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28  
L:1008 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29  
L:1011 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:29  
L:1023 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30  
L:1026 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:30  
L:1038 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31  
L:1041 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31  
L:1053 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32  
L:1056 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32  
L:1068 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33  
L:1071 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:33  
L:1083 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34  
L:1086 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34  
L:1098 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:35  
L:1101 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35  
L:1113 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:36  
L:1116 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36  
L:1128 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:37  
L:1131 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37  
L:1143 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:38  
L:1146 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38  
L:1158 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:39  
L:1161 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39  
L:1173 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:40  
L:1176 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40  
L:1188 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:41  
L:1191 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41  
L:1203 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:42  
L:1206 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:42  
L:1218 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:43  
L:1221 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43  
L:1233 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:44  
L:1236 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44  
L:1248 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:45  
L:1251 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45  
L:1263 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:46  
L:1266 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:46  
L:1278 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:47  
L:1281 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:47  
L:1293 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:48  
L:1296 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48  
L:1308 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:49  
L:1311 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:49  
L:1323 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:50  
L:1326 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:50



## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/731,261

DATE: 06/05/2002

TIME: 10:14:18

Input Set : A:\ptoms.TXT

Output Set: N:\CRF3\06052002\I731261.raw

L:1338 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:51  
L:1341 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:51  
L:1353 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:52  
L:1356 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:52  
L:1371 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:53

<210> 7

<211> 20

<212> DNA

<213> Artificial

— see item #11 on

<400> 7

ctgtgtcagc acgcacgtta

ERROR summary SHEET.

20

Note: When Artificial Sequence is  
used for numeric identifier <213> use  
of <220>, <223> are mandatory.

<210> 3  
<211> 20  
<212> DNA  
<213> Artificial

See item # 11 on Error Summary Sheet.

<220>  
<221> primer  
<222> (1)..(20)  
<223>

note: when Artificial Sequence is used in numeric identifier <213>, use of <220> and <223> are mandatory.

<400> 3  
gcggggcggt gcgtgactac

Numeric Identifier <221> and <222> are not necessary when numeric identifier <213> is Artificial Sequence.

<210> 4  
<211> 24  
<212> DNA  
<213> Artificial

primer for response to numeric identifier <223> is OK.

<220>  
<221> primer  
<222> (1)..(24)  
<223>

<400> 4  
aggcaagggg gaagagaagg atgt



The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

24

<210> 5  
<211> 35  
<212> DNA  
<213> Artificial

<220>  
<221> primer  
<222> (1)..(35)  
<223>

<400> 5  
aagctgaagc cgaatttcct tgggatacca gagga

35

<210> 6  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> primer  
<222> (1)..(20)  
<223>

<400> 6